

SEQUENCE LISTING

<110> Butcher, Eugene C.
Campbell, James J.
Rottman, James B.
Wu, Lijan

<120> Modulation of Systemic Memory T Cell
Trafficking

<130> STAN-110CON

<140> Unassigned

<141> 2001-04-17

<150> 09/232,878

<151> 1999-01-15

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1677

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (183)...(1265)

<223> CCR4, Chemokine receptor coding sequence

<400> 1
cggggggtttt gatcttcttc cccttctttt ctcccccttc ttctttcctt cctccctccc 60
tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc 120
agaaaagcaa gctgcttctg gttgggcca gacctgcctt gaggagcctg tagagttaaa 180
aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
Met Asn Pro Thr Asp Ile Ala Asp Thr Leu Asp Glu Ser Ile
1 5 10 15
tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
20 25 30
gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
35 40 45
ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
50 55 60
ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
65 70 75
aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467

Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp	80	85	90	95	
ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag					515
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys	100		105	110	
atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt					563
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe	115		120	125	
gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg					611
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val	130		135	140	
ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg					659
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu	145		150	155	
gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc					707
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe	160	165	170	175	
agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac					755
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr	180		185	190	
tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac					803
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn	195		200	205	
att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc					851
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser	210		215	220	
atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag					899
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys	225	230	235		
gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg					947
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp	240	245	250	255	
aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa					995
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu	260		265	270	
gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag					1043
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln	275		280	285	
gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc					1091
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile	290		295	300	
tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc					1139
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe	305	310	315		

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187
 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu 335
 320 325 330 335

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc 1235
 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr 350
 340 345 350

atg gat cat gat ctt cat gat gct ctg tag gaaaaatgaa atgggtgaaat 1285
 Met Asp His Asp Leu His Asp Ala Leu *
 355 360

gcagagtcaa tgaacttttc cacattcaga gcttacttta aaattggtat ttttaggtaa 1345
 gagatccctg agccagtgtc aggaggaagg cttacaccca cagtggaaag acagcttctc 1405
 atcctgcagg cagctttttc tctcccacta gacaagtcca gcctggcaag gggtcacctg 1465
 ggctgaggca tccttctctca caccaggctt gcctgcaggc atgagtcagt ctgatgagaa 1525
 ctctgagcag tgcttgaatg aagttgtagg taatattgca aggcaaagac tattcccttc 1585
 taacctgaac tgatggggtt ctccagaggg aattgcagag tactggctga tggagtaa 1645
 cgctaccttt tgctgtggca aatgggcccc cg 1677

<210> 2
 <211> 360
 <212> PRT
 <213> H. sapiens

<400> 2
 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
 1 5 10 15
 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
 20 25 30
 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45
 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
 50 55 60
 Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80
 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
 85 90 95
 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
 100 105 110
 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
 115 120 125
 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 130 135 140
 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
 145 150 155 160
 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175
 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190
 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205
 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220
 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240
 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr

245 250 255
 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270
 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285
 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300
 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320
 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335
 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350
 Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 3
 <211> 538
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (53)...(337)
 <223> Coding sequence for TARC chemokine

<400> 3 58
 ccctgagcag agggacctgc acacagagac tccctcctgg gctcctggca cc atg gcc
 Met Ala
 1

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
 Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
 5 10 15

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
 Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
 20 25 30

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
 Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
 35 40 45 50

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
 Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
 55 60 65

gtg cag ggc agg gcc atc tgt tgc gac ccc aac aac aag aga gtg aag 298
 Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
 70 75 80

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga agcctcctca 347
 Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser *
 85 90

cccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tgttcaccgc 407
 cccacacctg agcgccctggg tccaggggag gccttccagg gacgaagaag agccacagtg 467
 agggagatcc catccccttg tctgaactgg agccatgggc acaaagggcc cagattaaag 527

```
<210> 4
<211> 94
<212> PRT
<213> H. sapiens
```

[illegible]

```
<210> 5
<211> 2923
<212> DNA
<213> H. sapiens
```

```
<220>  
<221> CDS  
<222> (20)...(301)  
<223> Coding sequence for MDC chemokine
```

[illegible]

aggctcagga	gccctacctc	cctgccatta	tagctgctcc	ccgccagaag	cctgtgccaa	401
ctctctgcat	tccctgatct	ccatccctgt	ggctgtcacc	cttgggtcacc	tccgtgctgt	461
cactgccatc	tccccctga	cccctctaac	ccatcctctg	cctccctccc	tgcagtcaga	521
gggtcctggt	cccacagcg	attccccctgc	ttaaaccctt	ccatgactcc	ccactgccct	581
aagctgaggt	cagtctccca	agcctggcat	gtggccctct	ggatctgggt	tccatctctg	641
tctccagcct	gccacttcc	cttcatgaat	gttgggttct	agctccctgt	tctccaaacc	701
catactacac	atcccacttc	tgggtctttg	cctgggatgt	tgtgacact	cagaaagtcc	761
caccacctgc	acatgtgtag	ccccaccagc	cctccaaggc	attgctcgcc	caagcagctg	821
gtaattccat	ttcatgtatt	agatgtcccc	tggccctctg	tccctcttta	ataaccctag	881
tcacagtctc	cgcagattct	tgggatttgg	gggttttctc	ccccacctct	ccactagtgt	941
gaccaaggtt	tctagctaag	ttactctagt	ctccaagcct	ctagcataga	gcaactgcaga	1001
caggccctgg	ctcagaatca	gagcccagaa	agtggctgca	gacaaaatca	ataaaaactaa	1061
tgtccctccc	ctctccctgc	caaaaaggcag	ttacatatca	atacagagac	tcaagggtcac	1121
tagaaatggg	ccagctgggt	caatgtgaag	ccccaaattt	gccagatttc	acctttcttc	1181
ccccactccc	tttttttttt	tttttttttt	gagatggagt	ttcgtctctg	tcacccacgc	1241
tggagtgcga	tgggtgtggtc	ttggcttatt	gaagcctctg	cctcctgggt	tcaagtgtatt	1301
ctcttgctc	agcctcctga	gtagctggga	ttacagggtc	ctgctaccac	gccagctaa	1361
tttttgtatt	tttagtagag	acgaggcttc	accatgttgg	ccaggctggt	ctcgaactcc	1421
tgtcctcagg	taatccgccc	acctcagcct	cccaaagtgc	tgggattaca	ggcgtgagcc	1481
acagtgcctg	gcctcttccc	tctccccact	gcccccccca	actttttttt	tttttttatg	1541
gcagggtctc	actctgtcgc	ccaggctgga	gtgcagtggc	gtgatctcgg	ctcactacaa	1601
cctcgacctc	ctgggttcaa	gtgattctcc	caccccagcc	tcccaagtag	ctgggattac	1661
agggtgtgtc	cactacgggt	ggctaatttt	tgtattttta	gtagagacag	gtttcaccat	1721
attggccagg	ctggtcttga	actcctgacc	tcaagtgtac	caccttcctt	gtgctcccaa	1781
agtgtgaga	ttacaggcgt	gagctatcac	accagcctc	cccccttttt	tcctaatagg	1841
agactcctgt	acctttcttc	gttttaccta	tgtgtcgtgt	ctgcttacat	ttccttctcc	1901
cctcaggctt	tttttgggtg	gtcctccaac	ctccaatacc	caggcctggc	ctcttcagag	1961
taccccccat	tccacttttc	ctgcctcctt	ccttaaatag	ctgacaatca	aattcatgct	2021
atgggtgtgaa	agactacctt	tgacttggta	ttataagctg	gagttatata	tgtatttgaa	2081
aacagagtaa	atacttaaga	ggccaaatag	atgaatggaa	gaattttagg	aactgtgaga	2141
gggggacaag	gtgaagcttt	cctggccctg	ggaggaagct	ggctgtggta	gcgtagcgt	2201
ctctctctct	gtctgtggca	ggagccaaag	agtaggggtg	aattgagtga	aggaatcctg	2261
ggtagagacc	attctcaggt	ggttgggcca	ggctaaagac	tgggagttgg	gtctatctat	2321
gcctttctgg	ctgatttttg	tagagacggg	gttttgccat	gttaccagg	ctgggtctcaa	2381
actcctgggc	tcaagcgatc	ctcctggctc	agcctcccaa	agtgtggga	ttacaggcgt	2441
gaatcactgc	gcctggcttc	ctcttcctct	tgagaaatat	tcttttcata	cagcaagtat	2501
gggacagcag	tgtcccaggt	aaaggacata	aatgttacaa	gtgtctggtc	ctttctgagg	2561
gaggctgggtg	ccgctctgca	gggtatttga	acctgtggaa	ttggaggagg	ccatttcact	2621
ccctgaaccc	agcctgacaa	atcacagtga	gaatgttcac	cttataggct	tgtgtggggg	2681
ctcaggttga	aagtgtgggg	agtgcactg	cctaggcatc	cagctcagtg	tcacccaggg	2741
cctgtgtccc	tcccgaaccc	aggggtcaacc	tgcctgccac	aggcactaga	aggacgaatc	2801
tgcctactgc	ccatgaacgg	ggccctcaag	cgtcctggga	tctccttctc	cctcctgtcc	2861
tgtccttgcc	cctcaggact	gctggaaaat	aatccttta	aaatagtaaa	aaaaaaaaaa	2921
aa						2923

<210> 6
 <211> 93
 <212> PRT
 <213> H. sapiens

<400> 6
 Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
 1 5 10 15
 Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
 20 25 30
 Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 35 40 45

Val	Val	Lys	His	Phe	Tyr	Trp	Thr	Ser	Asp	Ser	Cys	Pro	Arg	Pro	Gly
	50					55					60				
Val	Val	Leu	Leu	Thr	Phe	Arg	Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Arg
65					70					75					80
Val	Pro	Trp	Val	Lys	Met	Ile	Leu	Asn	Lys	Leu	Ser	Gln			
				85					90						

TDZTD = 94426350